SEQUENCE LISTING

<110> Sauter, Margret M
Lorbiecke, Rene

<120> ALTERATION OF GROWTH AND ADAPTATION UNDER HYPOXIC CONDITIONS

<130> 2283/201

<140> 09/785,738
<141> 2001-02-16

<150> 60/183,572
<151> 2000-02-18

<160> 18

<170> PatentIn Ver. 2.1

<210> 1
<211> 872
<212> DNA
<213> Rice

<220>
<221> CDS
<222> (69)..(668)

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caatccac atg gag aac gaa ttc cag gat ggt aag acg gag gtg ata gaa 110
Met Glu Asn Glu Phe Gln Asp Gly Lys Thr Glu Val Ile Glu
1 5 10

gca tgg tac atg gat gat agc gaa gag gac cag agg ctt cct cat cac 158
Ala Trp Tyr Met Asp Asp Ser Glu Glu Asp Gln Arg Leu Pro His His
15 20 25 30

cgc gaa ccc aaa gaa ttc att cct gtt gat aag ctt aca gaa cta gga 206
Arg Glu Pro Lys Glu Phe Ile Pro Val Asp Lys Leu Thr Glu Leu Gly
35 40 45

gta atc agc tgg cgc cta aat cct gat aac tgg gag aat tgc gag aac 254
Val Ile Ser Trp Arg Leu Asn Pro Asp Asn Trp Glu Asn Cys Glu Asn
50 55 60

ctg aag aga atc cgc gaa gcc aga ggt tac tct tat gtg gac att tgt 302
Leu Lys Arg Ile Arg Glu Ala Arg Gly Tyr Ser Tyr Val Asp Ile Cys
65 70 75

gat gtg tgc cca gag aag ctg cca aat tat gaa act aag atc aag agt 350
Asp Val Cys Pro Glu Lys Leu Pro Asn Tyr Glu Thr Lys Ile Lys Ser
80 85 90

ttc ttt gaa gaa cac ctg cat acc gat gaa gaa ata cgc tat tgt ctt 398
Phe Phe Glu Glu His Leu His Thr Asp Glu Glu Ile Arg Tyr Cys Leu
95 100 105 110

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gaa ggg agt gga tac ttt gat gtg aga gac caa aat gat cag tgg att   446
Glu Gly Ser Gly Tyr Phe Asp Val Arg Asp Gln Asn Asp Gln Trp Ile
                115                 120                 125

cgt ata gca ctg aag aaa gga ggc atg att gtt ctg cct gca ggg atg   494
Arg Ile Ala Leu Lys Lys Gly Gly Met Ile Val Leu Pro Ala Gly Met
            130                 135                 140

tac cac cgc ttt acg ttg gac acc gac aac tat atc aag gca atg cga   542
Tyr His Arg Phe Thr Leu Asp Thr Asp Asn Tyr Ile Lys Ala Met Arg
        145                 150                 155

ctg ttt gtt ggc gat cct gtt tgg aca ccc tac aac cgt ccc cat gac   590
Leu Phe Val Gly Asp Pro Val Trp Thr Pro Tyr Asn Arg Pro His Asp
    160                 165                 170

cat ctt cct gca aga aag gag ttt ttg gct aaa ctt ctc aag tca gaa   638
His Leu Pro Ala Arg Lys Glu Phe Leu Ala Lys Leu Leu Lys Ser Glu
175                 180                 185                 190

ggt gaa aat caa gca gtt gaa ggc ttc tga gggttttgtt gggctcctgc     688
Gly Glu Asn Gln Ala Val Glu Gly Phe
                195                 200

actgcggttc tatattcaac ctgaataaga tgtgctatag caatgtaaat ttagcacagt 748

ggctatggtc gccactcacc aacttgaagt gaaagattta atgatttttg ttaattctta 808

tgtatcaatc ggcatatagc atttccgaaa tgtgttttca ataaacagga gtcatgaagc 868

tgaa                                                              872


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<212> PRT
<213> Rice

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             20                  25                  30
Pro Lys Glu Phe Ile Pro Val Asp Lys Leu Thr Glu Leu Gly Val Ile
         35                  40                  45
Ser Trp Arg Leu Asn Pro Asp Asn Trp Glu Asn Cys Glu Asn Leu Lys
     50                  55                  60
Arg Ile Arg Glu Ala Arg Gly Tyr Ser Tyr Val Asp Ile Cys Asp Val
 65                  70                  75                  80
Cys Pro Glu Lys Leu Pro Asn Tyr Glu Thr Lys Ile Lys Ser Phe Phe
                 85                  90                  95
Glu Glu His Leu His Thr Asp Glu Glu Ile Arg Tyr Cys Leu Glu Gly
            100                 105                 110
Ser Gly Tyr Phe Asp Val Arg Asp Gln Asn Asp Gln Trp Ile Arg Ile
        115                 120                 125
Ala Leu Lys Lys Gly Gly Met Ile Val Leu Pro Ala Gly Met Tyr His
    130                 135                 140
Arg Phe Thr Leu Asp Thr Asp Asn Tyr Ile Lys Ala Met Arg Leu Phe
145                 150                 155                 160
Val Gly Asp Pro Val Trp Thr Pro Tyr Asn Arg Pro His Asp His Leu
                165                 170                 175
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Pro Ala Arg Lys Glu Phe Leu Ala Lys Leu Leu Lys Ser Glu Gly Glu
            180                 185                 190
Asn Gln Ala Val Glu Gly Phe
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<222> (139)..(735)

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aggctatccg gaatcgggag ggtttcccaa taggaaagca actcaggact caggagcggc 120

gtctgagagg tttcagag atg gag aac cag ttc cag gat ggc aag gag gag   171
                    Met Glu Asn Gln Phe Gln Asp Gly Lys Glu Glu
                      1               5                  10

gtc atc gaa gct tgg tac atg gat gac agt gaa gag gac cag agg ctt   219
Val Ile Glu Ala Trp Tyr Met Asp Asp Ser Glu Glu Asp Gln Arg Leu
             15                  20                  25

cct cat cat cgt gag ccc aaa gaa ttc att cct ctt agc aaa ctt tca   267
Pro His His Arg Glu Pro Lys Glu Phe Ile Pro Leu Ser Lys Leu Ser
         30                  35                  40

gag tta gga ata tta agc tgg cgc ctg aat gct gat gac tgg gag aat   315
Glu Leu Gly Ile Leu Ser Trp Arg Leu Asn Ala Asp Asp Trp Glu Asn
     45                  50                  55

gat gag aac ctc aag aaa atc cgt gag gcc agg gga tac tct tac atg   363
Asp Glu Asn Leu Lys Lys Ile Arg Glu Ala Arg Gly Tyr Ser Tyr Met
 60                  65                  70                  75

gat att tgt gat gtg tgt cca gaa aag ctg cca aac tat gag gct aag   411
Asp Ile Cys Asp Val Cys Pro Glu Lys Leu Pro Asn Tyr Glu Ala Lys
                 80                  85                  90

ctg aaa aat ttc ttt gaa gaa cac ttg cat act gat gaa gag ata cgc   459
Leu Lys Asn Phe Phe Glu Glu His Leu His Thr Asp Glu Glu Ile Arg
             95                  100                 105

tat tgt ctt gag gga agt gga tac ttc gat gtc agg gac caa aat gat   507
Tyr Cys Leu Glu Gly Ser Gly Tyr Phe Asp Val Arg Asp Gln Asn Asp
        110                 115                 120

cag tgg atc cgt gta gca gtg aag aaa ggg ggc atg att gtt ttg cct   555
Gln Trp Ile Arg Val Ala Val Lys Lys Gly Gly Met Ile Val Leu Pro
    125                 130                 135

gcg gga atg tat cac cgc ttc aca ttg gac agt gac aac tac atc aag   603
Ala Gly Met Tyr His Arg Phe Thr Leu Asp Ser Asp Asn Tyr Ile Lys
140                 145                 150                 155
```

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gca atg cgg ctc ttt gtg gga gag cct gtc tgg acg ccg tac aac cgt   651
Ala Met Arg Leu Phe Val Gly Glu Pro Val Trp Thr Pro Tyr Asn Arg
                160                 165                 170

ccc cat gac cat ctg cca gct aga aag gag tat gtc gaa aaa att atc   699
Pro His Asp His Leu Pro Ala Arg Lys Glu Tyr Val Glu Lys Ile Ile
            175                 180                 185

aac agg ggt gga act caa gct gtc gaa gct cgt taa aggcatatca        745
Asn Arg Gly Gly Thr Gln Ala Val Glu Ala Arg
        190                 195

agatgtgctt cctagttcgg tgttctgtta cactctacag atactgaata aactgtgcta 805

tcagctgttg caatgggctc ctaccgacat cttacatcat ttggcagtat tttgcacaaa 865

cccgcttaaa atctccctga aaatacgcac gtcaccatgt cagagtgttt atatacaata 925

atgacacttc agtccacagt cagcaaggga ctaatgacaa aaaaaaaaaa aaaaa      980
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             20                  25                  30
Pro Lys Glu Phe Ile Pro Leu Ser Lys Leu Ser Glu Leu Gly Ile Leu
         35                  40                  45
Ser Trp Arg Leu Asn Ala Asp Asp Trp Glu Asn Asp Glu Asn Leu Lys
     50                  55                  60
Lys Ile Arg Glu Ala Arg Gly Tyr Ser Tyr Met Asp Ile Cys Asp Val
 65                  70                  75                  80
Cys Pro Glu Lys Leu Pro Asn Tyr Glu Ala Lys Leu Lys Asn Phe Phe
                 85                  90                  95
Glu Glu His Leu His Thr Asp Glu Glu Ile Arg Tyr Cys Leu Glu Gly
            100                 105                 110
Ser Gly Tyr Phe Asp Val Arg Asp Gln Asn Asp Gln Trp Ile Arg Val
        115                 120                 125
Ala Val Lys Lys Gly Gly Met Ile Val Leu Pro Ala Gly Met Tyr His
    130                 135                 140
Arg Phe Thr Leu Asp Ser Asp Asn Tyr Ile Lys Ala Met Arg Leu Phe
145                 150                 155                 160
Val Gly Glu Pro Val Trp Thr Pro Tyr Asn Arg Pro His Asp His Leu
                165                 170                 175
Pro Ala Arg Lys Glu Tyr Val Glu Lys Ile Ile Asn Arg Gly Gly Thr
            180                 185                 190
Gln Ala Val Glu Ala Arg
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<210> 5
<211> 774
<212> DNA
<213> Tomato

<220>
<221> CDS
<222> (1)..(591)

<400> 5

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gca cca gat cca aga gag gat gtc ata cag gca tgg tac atg gat gac   48
Ala Pro Asp Pro Arg Glu Asp Val Ile Gln Ala Trp Tyr Met Asp Asp
  1               5                  10                  15

aac gat gag gac cag agg ctt cct cat cac cgt gag cca aag gaa ttt   96
Asn Asp Glu Asp Gln Arg Leu Pro His His Arg Glu Pro Lys Glu Phe
             20                  25                  30

gtg tct ctt gac aag ctg gct gaa ctt gga gtg ctc agc tgg aga ctt   144
Val Ser Leu Asp Lys Leu Ala Glu Leu Gly Val Leu Ser Trp Arg Leu
         35                  40                  45

gat gct gac aat tat gag act gat gag gag ttg aag aaa att cgg gaa   192
Asp Ala Asp Asn Tyr Glu Thr Asp Glu Glu Leu Lys Lys Ile Arg Glu
     50                  55                  60

gat cgt gga tat tca tac att gat ttc tgt gag gtt tgc cct gag aaa   240
Asp Arg Gly Tyr Ser Tyr Ile Asp Phe Cys Glu Val Cys Pro Glu Lys
 65                  70                  75                  80

cta ccg aat tac gag gag aaa atc aag aac ttt ttt gaa gaa cac ctg   288
Leu Pro Asn Tyr Glu Glu Lys Ile Lys Asn Phe Phe Glu Glu His Leu
                 85                  90                  95

cac acc gac gag gag atc cgt tac gct gtt gca gga agt ggt tac ttt   336
His Thr Asp Glu Glu Ile Arg Tyr Ala Val Ala Gly Ser Gly Tyr Phe
            100                 105                 110

gat gtc cgc gat gtg aat gag agc tgg att cgc gtc tgg gta aag aaa   384
Asp Val Arg Asp Val Asn Glu Ser Trp Ile Arg Val Trp Val Lys Lys
        115                 120                 125

ggt gga atg att gtt ctt cct gct gga atc tat cac cgc ttc acg ctt   432
Gly Gly Met Ile Val Leu Pro Ala Gly Ile Tyr His Arg Phe Thr Leu
    130                 135                 140

gat tca agc aac tac att aag gca atg cgt ctc ttt gtt ggt gac cca   480
Asp Ser Ser Asn Tyr Ile Lys Ala Met Arg Leu Phe Val Gly Asp Pro
145                 150                 155                 160

att tgg act cca tac aat cgt cca cat gat cat ctt ccc gca agg caa   528
Ile Trp Thr Pro Tyr Asn Arg Pro His Asp His Leu Pro Ala Arg Gln
                165                 170                 175

gaa tat gtt gag acg ttt gtc aac gca gat ggc gct ggt cgt gct gtt   576
Glu Tyr Val Glu Thr Phe Val Asn Ala Asp Gly Ala Gly Arg Ala Val
            180                 185                 190

aat gct gct gct taa atcaactata ggagaggaat ttgaaatcgt actagattgt   631
Asn Ala Ala Ala
        195

aataaatatt accatatggt ggctttgctg ttcttgatgt gtgccttact aagcatgttt 691

aatgttgtat tgtggcacta ataaaatcac cccctatggg agattgattg tttatatgca 751
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agtggaattt attatgtgat ttt 774

<210> 6
<211> 196
<212> PRT
<213> Tomato

<400> 6

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Asn Asp Glu Asp Gln Arg Leu Pro His His Arg Glu Pro Lys Glu Phe
            20                  25                  30
Val Ser Leu Asp Lys Leu Ala Glu Leu Gly Val Leu Ser Trp Arg Leu
        35                  40                  45
Asp Ala Asp Asn Tyr Glu Thr Asp Glu Glu Leu Lys Lys Ile Arg Glu
    50                  55                  60
Asp Arg Gly Tyr Ser Tyr Ile Asp Phe Cys Glu Val Cys Pro Glu Lys
65                  70                  75                  80
Leu Pro Asn Tyr Glu Glu Lys Ile Lys Asn Phe Phe Glu Glu His Leu
                85                  90                  95
His Thr Asp Glu Glu Ile Arg Tyr Ala Val Ala Gly Ser Gly Tyr Phe
            100                 105                 110
Asp Val Arg Asp Val Asn Glu Ser Trp Ile Arg Val Trp Val Lys Lys
        115                 120                 125
Gly Gly Met Ile Val Leu Pro Ala Gly Ile Tyr His Arg Phe Thr Leu
    130                 135                 140
Asp Ser Ser Asn Tyr Ile Lys Ala Met Arg Leu Phe Val Gly Asp Pro
145                 150                 155                 160
Ile Trp Thr Pro Tyr Asn Arg Pro His Asp His Leu Pro Ala Arg Gln
                165                 170                 175
Glu Tyr Val Glu Thr Phe Val Asn Ala Asp Gly Ala Gly Arg Ala Val
            180                 185                 190
Asn Ala Ala Ala
        195
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<210> 7
<211> 603
<212> DNA
<213> Tomato

<220>
<221> CDS
<222> (3)..(572)

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   Met Ala Ile Glu Cys Lys Ala Trp Phe Met Asp Glu Asn Ser Glu
     1               5                  10                  15

gat cag cgg cta ccg cac cag aag aac cca ccg gag ttt gtt tca gtg   95
Asp Gln Arg Leu Pro His Gln Lys Asn Pro Pro Glu Phe Val Ser Val
                20                  25                  30

gag aaa tta gca gta atc gga gtt tta tac tgg aaa ttg aac cct aat   143
Glu Lys Leu Ala Val Ile Gly Val Leu Tyr Trp Lys Leu Asn Pro Asn
            35                  40                  45

gat tac gag aac gat gaa gaa ttg aaa aaa att cgt caa agt aga ggc   191
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```
Asp Tyr Glu Asn Asp Glu Glu Leu Lys Lys Ile Arg Gln Ser Arg Gly
          50                  55                  60

tac agc tac atg gac ttg ctg gat ttg tgc cct gag aag gtg gat aac   239
Tyr Ser Tyr Met Asp Leu Leu Asp Leu Cys Pro Glu Lys Val Asp Asn
     65                  70                  75

tat gag cag aag ttg aaa aat ttc tat acg gag cac ata cac gca gat   287
Tyr Glu Gln Lys Leu Lys Asn Phe Tyr Thr Glu His Ile His Ala Asp
 80                  85                  90                  95

gag gag ata cgt tac tgt ctg gaa ggg agt gga tat ttt gat gtg aga   335
Glu Glu Ile Arg Tyr Cys Leu Glu Gly Ser Gly Tyr Phe Asp Val Arg
                100                 105                 110

gac aag gat gat cgc tgg att cgc atc tgg atg aag gcc ggt gat atg   383
Asp Lys Asp Asp Arg Trp Ile Arg Ile Trp Met Lys Ala Gly Asp Met
            115                 120                 125

att gtc ttg cct gct ggg att tac cac cgg ttc acc cta gat act gat   431
Ile Val Leu Pro Ala Gly Ile Tyr His Arg Phe Thr Leu Asp Thr Asp
        130                 135                 140

aac tat gtc aag ttg atg agg ttg ttt gtg gga gag ccg gtg tgg acg   479
Asn Tyr Val Lys Leu Met Arg Leu Phe Val Gly Glu Pro Val Trp Thr
    145                 150                 155

cct tac aat cga cca caa gaa gat cat cca gca agg aag gag tac atc   527
Pro Tyr Asn Arg Pro Gln Glu Asp His Pro Ala Arg Lys Glu Tyr Ile
160                 165                 170                 175

aag agt gtt act gaa aga gta gga gtg cct ctt aca gca cac taa       572
Lys Ser Val Thr Glu Arg Val Gly Val Pro Leu Thr Ala His
                180                 185                 190

gacatatttg agctttacaa acctgagagt g                               603


<210> 8
<211> 189
<212> PRT
<213> Tomato

<400> 8
Met Ala Ile Glu Cys Lys Ala Trp Phe Met Asp Glu Asn Ser Glu Asp
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             20                  25                  30
Lys Leu Ala Val Ile Gly Val Leu Tyr Trp Lys Leu Asn Pro Asn Asp
         35                  40                  45
Tyr Glu Asn Asp Glu Glu Leu Lys Lys Ile Arg Gln Ser Arg Gly Tyr
     50                  55                  60
Ser Tyr Met Asp Leu Leu Asp Leu Cys Pro Glu Lys Val Asp Asn Tyr
 65                  70                  75                  80
Glu Gln Lys Leu Lys Asn Phe Tyr Thr Glu His Ile His Ala Asp Glu
                 85                  90                  95
Glu Ile Arg Tyr Cys Leu Glu Gly Ser Gly Tyr Phe Asp Val Arg Asp
            100                 105                 110
Lys Asp Asp Arg Trp Ile Arg Ile Trp Met Lys Ala Gly Asp Met Ile
        115                 120                 125
Val Leu Pro Ala Gly Ile Tyr His Arg Phe Thr Leu Asp Thr Asp Asn
```

```
    130                 135                 140
Tyr Val Lys Leu Met Arg Leu Phe Val Gly Glu Pro Val Trp Thr Pro
145                 150                 155                 160
Tyr Asn Arg Pro Gln Glu Asp His Pro Ala Arg Lys Glu Tyr Ile Lys
                165                 170                 175
Ser Val Thr Glu Arg Val Gly Val Pro Leu Thr Ala His
            180                 185
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<210> 9
<211> 889
<212> DNA
<213> Soybean

<220>
<221> CDS
<222> (32)..(634)

<400> 9

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                                    Met Val Ser Ser Asp Lys Asp
                                      1               5

cca cga gag gat gtc ctt caa gcc tgg tac atg gat gat agt gat gaa   100
Pro Arg Glu Asp Val Leu Gln Ala Trp Tyr Met Asp Asp Ser Asp Glu
         10                  15                  20

gat caa aga ctc ccc cac cac aaa gaa ccc aag gag ttt gtc tcg ttg   148
Asp Gln Arg Leu Pro His His Lys Glu Pro Lys Glu Phe Val Ser Leu
     25                  30                  35

gac caa ctt gct gaa ctt gga gtc ctt agc tgg aaa cta gat gct gat   196
Asp Gln Leu Ala Glu Leu Gly Val Leu Ser Trp Lys Leu Asp Ala Asp
 40                  45                  50                  55

aac cat gaa aat gat cca gag ctg aag aag att cgt gaa gag cgt ggt   244
Asn His Glu Asn Asp Pro Glu Leu Lys Lys Ile Arg Glu Glu Arg Gly
                 60                  65                  70

tac acc tac atg gat gtt tgt gag gtc tgc cca gaa aag ttg cca aat   292
Tyr Thr Tyr Met Asp Val Cys Glu Val Cys Pro Glu Lys Leu Pro Asn
             75                  80                  85

tat gaa cag aaa atc aaa agc ttc ttt gaa gag cat ctt cac act gat   340
Tyr Glu Gln Lys Ile Lys Ser Phe Phe Glu Glu His Leu His Thr Asp
         90                  95                  100

gag gag atc cgc ttt tgt gct gct gga agt ggc tat ttt gat gtt agg   388
Glu Glu Ile Arg Phe Cys Ala Ala Gly Ser Gly Tyr Phe Asp Val Arg
    105                 110                 115

gat cgc aat gaa gct tgg att cgt gtg tgg gtc aag aaa gga gga atg   436
Asp Arg Asn Glu Ala Trp Ile Arg Val Trp Val Lys Lys Gly Gly Met
120                 125                 130                 135

atc atc tta cct gcc gga att tat cat cgc ttt acg cta gat gag agc   484
Ile Ile Leu Pro Ala Gly Ile Tyr His Arg Phe Thr Leu Asp Glu Ser
                140                 145                 150

aac tac att aag gct ttg cgt ttt ttt gtt ggt gag cca gtt tgg act   532
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Asn Tyr Ile Lys Ala Leu Arg Phe Phe Val Gly Glu Pro Val Trp Thr
155 160 165

cca tac aat cgt cca aat gac cat ctc cct gca aga caa caa tat gtc 580
Pro Tyr Asn Arg Pro Asn Asp His Leu Pro Ala Arg Gln Gln Tyr Val
170 175 180

aag gat ttt gtg gaa aag gat gtt agc agc cat gct gtt gat gcc acc 628
Lys Asp Phe Val Glu Lys Asp Val Ser Ser His Ala Val Asp Ala Thr
185 190 195

gcg taa gatctggttc tgcctaatca tagtaccaca tgaaaaggac caagactttg 684
Ala
200

ttgctaaagt aaggtttgaa aaaaagaaaa taatggtgtc tttaaataaa gggtcctggc 744

ttgttatgcc ttgatgtacc ctcgccagtg tttttgttgc ctgtccctgt ataaagattg 804

cattgtatta ttattagaat tgggtacaga ataaacataa gcataagtta gcatgctgat 864

gtatatttat gtaaaaaaaa ataaa 889

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<211> 200
<212> PRT
<213> Soybean

<400> 10
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Tyr Met Asp Asp Ser Asp Glu Asp Gln Arg Leu Pro His His Lys Glu
20 25 30
Pro Lys Glu Phe Val Ser Leu Asp Gln Leu Ala Glu Leu Gly Val Leu
35 40 45
Ser Trp Lys Leu Asp Ala Asp Asn His Glu Asn Asp Pro Glu Leu Lys
50 55 60
Lys Ile Arg Glu Glu Arg Gly Tyr Thr Tyr Met Asp Val Cys Glu Val
65 70 75 80
Cys Pro Glu Lys Leu Pro Asn Tyr Glu Gln Lys Ile Lys Ser Phe Phe
85 90 95
Glu Glu His Leu His Thr Asp Glu Glu Ile Arg Phe Cys Ala Ala Gly
100 105 110
Ser Gly Tyr Phe Asp Val Arg Asp Arg Asn Glu Ala Trp Ile Arg Val
115 120 125
Trp Val Lys Lys Gly Gly Met Ile Ile Leu Pro Ala Gly Ile Tyr His
130 135 140
Arg Phe Thr Leu Asp Glu Ser Asn Tyr Ile Lys Ala Leu Arg Phe Phe
145 150 155 160
Val Gly Glu Pro Val Trp Thr Pro Tyr Asn Arg Pro Asn Asp His Leu
165 170 175
Pro Ala Arg Gln Gln Tyr Val Lys Asp Phe Val Glu Lys Asp Val Ser
180 185 190
Ser His Ala Val Asp Ala Thr Ala
195 200

<210> 11

<211> 933
<212> DNA
<213> Cotton

<220>
<221> CDS
<222> (33)..(635)

<400> 11

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                                    Met Thr Met Gly Ser Ala Asp
                                      1               5

aag agg gag gaa gtt att cag gca tgg tac atg gat gat agt gat gaa   101
Lys Arg Glu Glu Val Ile Gln Ala Trp Tyr Met Asp Asp Ser Asp Glu
         10                  15                  20

gat cag agg ctt cct cat cac cgt gaa cct aag gaa tat gta tcc ttg   149
Asp Gln Arg Leu Pro His His Arg Glu Pro Lys Glu Tyr Val Ser Leu
     25                  30                  35

gat aaa ctt gct gag ctt gga gta ctc agc tgg cga ttg gat gct gat   197
Asp Lys Leu Ala Glu Leu Gly Val Leu Ser Trp Arg Leu Asp Ala Asp
 40                  45                  50                  55

aac tat gaa aat gat gaa gag ttg aag aaa att cgt gaa gaa cga ggt   245
Asn Tyr Glu Asn Asp Glu Glu Leu Lys Lys Ile Arg Glu Glu Arg Gly
                 60                  65                  70

tac tcc tac atg gac ttc tgc gag gtt tgc cct gag aag ctt cca aat   293
Tyr Ser Tyr Met Asp Phe Cys Glu Val Cys Pro Glu Lys Leu Pro Asn
             75                  80                  85

tat gag gag aag ata aaa aat ttc ttc gaa gaa cat att cat act gat   341
Tyr Glu Glu Lys Ile Lys Asn Phe Phe Glu Glu His Ile His Thr Asp
         90                  95                  100

gag gag atc cgt tac tgt gtg gca gga agt ggt tat ttt gat gta cgg   389
Glu Glu Ile Arg Tyr Cys Val Ala Gly Ser Gly Tyr Phe Asp Val Arg
    105                 110                 115

gat cat aat gat aaa tgg att cgt gtg tgg gtg aag aaa gga ggc atg   437
Asp His Asn Asp Lys Trp Ile Arg Val Trp Val Lys Lys Gly Gly Met
120                 125                 130                 135

ata gtt tta cct gct gga att tat cat cgc ttt act ctg gat aca gac   485
Ile Val Leu Pro Ala Gly Ile Tyr His Arg Phe Thr Leu Asp Thr Asp
                140                 145                 150

aac tat att aag gca atg cgg ctc ttt gtt ggt gat cca att tgg act   533
Asn Tyr Ile Lys Ala Met Arg Leu Phe Val Gly Asp Pro Ile Trp Thr
            155                 160                 165

ccg tac aat cgt ccg cac gat cat ctt cct gca agg aag gag tat atc   581
Pro Tyr Asn Arg Pro His Asp His Leu Pro Ala Arg Lys Glu Tyr Ile
        170                 175                 180


aag aac ttt ttg cgg gag gaa ggt ggt ggc caa gcc gtt gat gct gcc   629
Lys Asn Phe Leu Arg Glu Glu Gly Gly Gly Gln Ala Val Asp Ala Ala
    185                 190                 195
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gca taa aatcaacatt catctggtgg tggccaagtc gttgatgctg ccgcataaaa 685
Ala
200

tcagcattca tctctggtat cgtgtcttat aaaatatgaa accccggatt tgtggtaata 745

aataagtcta ggcttgtctg cttttgatgc gtggatatgg atcgttatgg ttgttgcttg 805

ctatatattg cctattccat atcgaaaatt cgcaaacttg ctatgtattt ctacatttta 865

tgtgcttact accagattgg ctcttaataa tcaaagttta cataatatac atttcgtcga 925

cgcggccg 933

<210> 12
<211> 200
<212> PRT
<213> Cotton

<400> 12

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Met Thr Met Gly Ser Ala Asp Lys Arg Glu Glu Val Ile Gln Ala Trp
  1               5                  10                  15
Tyr Met Asp Asp Ser Asp Glu Asp Gln Arg Leu Pro His His Arg Glu
             20                  25                  30
Pro Lys Glu Tyr Val Ser Leu Asp Lys Leu Ala Glu Leu Gly Val Leu
         35                  40                  45
Ser Trp Arg Leu Asp Ala Asp Asn Tyr Glu Asn Asp Glu Glu Leu Lys
     50                  55                  60
Lys Ile Arg Glu Glu Arg Gly Tyr Ser Tyr Met Asp Phe Cys Glu Val
 65                  70                  75                  80
Cys Pro Glu Lys Leu Pro Asn Tyr Glu Glu Lys Ile Lys Asn Phe Phe
                 85                  90                  95
Glu Glu His Ile His Thr Asp Glu Glu Ile Arg Tyr Cys Val Ala Gly
            100                 105                 110
Ser Gly Tyr Phe Asp Val Arg Asp His Asn Asp Lys Trp Ile Arg Val
        115                 120                 125
Trp Val Lys Lys Gly Gly Met Ile Val Leu Pro Ala Gly Ile Tyr His
    130                 135                 140
Arg Phe Thr Leu Asp Thr Asp Asn Tyr Ile Lys Ala Met Arg Leu Phe
145                 150                 155                 160
Val Gly Asp Pro Ile Trp Thr Pro Tyr Asn Arg Pro His Asp His Leu
                165                 170                 175
Pro Ala Arg Lys Glu Tyr Ile Lys Asn Phe Leu Arg Glu Glu Gly Gly
            180                 185                 190
Gly Gln Ala Val Asp Ala Ala Ala
        195                 200
```

<210> 13
<211> 920
<212> DNA
<213> Human

<220>
<221> CDS
<222> (1)..(564)

<400> 13

```
cga aca cgg cac ccg cac tgc gcg tca gtg gtg cag gcc tgg tat atg   48
Arg Thr Arg His Pro His Cys Ala Ser Val Val Gln Ala Trp Tyr Met
  1               5                  10                  15

gac gac gcc ccg ggc acc cgc ggc aac ccc acc gcc ccg acc ccg gcc   96
Asp Asp Ala Pro Gly Thr Arg Gly Asn Pro Thr Ala Pro Thr Pro Ala
            20                  25                  30

gcc cag tgc gct gga gca gct gcg cgg ctc ggg gtg ctc tac tgg aag   144
Ala Gln Cys Ala Gly Ala Ala Ala Arg Leu Gly Val Leu Tyr Trp Lys
        35                  40                  45

ctg gat gct gac aaa tat gag aat gat cca gaa tta gaa aag atc cga   192
Leu Asp Ala Asp Lys Tyr Glu Asn Asp Pro Glu Leu Glu Lys Ile Arg
    50                  55                  60

aga gag agg aac tac tcc tgg atg gac atc ata acc ata tgc aaa gat   240
Arg Glu Arg Asn Tyr Ser Trp Met Asp Ile Ile Thr Ile Cys Lys Asp
65                  70                  75                  80

aaa cta cca aat tat gaa gaa aag att aag atg ttc tac gag gag cat   288
Lys Leu Pro Asn Tyr Glu Glu Lys Ile Lys Met Phe Tyr Glu Glu His
                85                  90                  95

ttg cac ttg gac gat gag atc cgc tac atc ctg gat ggc agt ggg tac   336
Leu His Leu Asp Asp Glu Ile Arg Tyr Ile Leu Asp Gly Ser Gly Tyr
            100                 105                 110

ttc gat gtg agg gac aag gag gac cag tgg atc cgg atc ttc atg gag   384
Phe Asp Val Arg Asp Lys Glu Asp Gln Trp Ile Arg Ile Phe Met Glu
        115                 120                 125

aag gga gac atg gtg acg ctc ccc gcg ggg atc tat cac cgc ttc acg   432
Lys Gly Asp Met Val Thr Leu Pro Ala Gly Ile Tyr His Arg Phe Thr
    130                 135                 140

gtg gac gag aag aac tac acg aag gcc atg cgg ctg ttt gtg gga gaa   480
Val Asp Glu Lys Asn Tyr Thr Lys Ala Met Arg Leu Phe Val Gly Glu
145                 150                 155                 160

ccg gtg tgg aca gcg tac aac cgg ccc gct gac cat ttt gaa gcc cgc   528
Pro Val Trp Thr Ala Tyr Asn Arg Pro Ala Asp His Phe Glu Ala Arg
                165                 170                 175

ggg cag tac gtg aaa ttt ctg gca cag acc gcc tag cagtgctgcc        574
Gly Gln Tyr Val Lys Phe Leu Ala Gln Thr Ala
            180                 185

tgggaactaa cacgtgcctc gtaaaggtcc ccaatgtaat gaactgagca gaaaattcaa 634

tcaactttct ctttgctttt agaggatagc cttgaggtag attatctttc ctttgtaaga 694

ttatttgatc agaatatttt gtaatgaaag gatctagaaa gcaacttgga agtgtaaaga 754

gtcaccttca ttttctgtaa ctcaatcaag actggtgggt ccatggccct gtgttagttc 814

attgcattca ggttgagtcc caaatgaaag tttcatctcc cgaaatgcag ttccttagat 874

gcccatctgg acgtgaatgc cgcgcctgcg tgtaagaagg tgcaat               920
```

<210> 14
<211> 187
<212> PRT
<213> Human

<400> 14

```
Arg Thr Arg His Pro His Cys Ala Ser Val Val Gln Ala Trp Tyr Met
  1               5                  10                  15
Asp Asp Ala Pro Gly Thr Arg Gly Asn Pro Thr Ala Pro Thr Pro Ala
             20                  25                  30
Ala Gln Cys Ala Gly Ala Ala Ala Arg Leu Gly Val Leu Tyr Trp Lys
         35                  40                  45
Leu Asp Ala Asp Lys Tyr Glu Asn Asp Pro Glu Leu Glu Lys Ile Arg
     50                  55                  60
Arg Glu Arg Asn Tyr Ser Trp Met Asp Ile Ile Thr Ile Cys Lys Asp
 65                  70                  75                  80
Lys Leu Pro Asn Tyr Glu Glu Lys Ile Lys Met Phe Tyr Glu Glu His
                 85                  90                  95
Leu His Leu Asp Asp Glu Ile Arg Tyr Ile Leu Asp Gly Ser Gly Tyr
            100                 105                 110
Phe Asp Val Arg Asp Lys Glu Asp Gln Trp Ile Arg Ile Phe Met Glu
        115                 120                 125
Lys Gly Asp Met Val Thr Leu Pro Ala Gly Ile Tyr His Arg Phe Thr
    130                 135                 140
Val Asp Glu Lys Asn Tyr Thr Lys Ala Met Arg Leu Phe Val Gly Glu
145                 150                 155                 160
Pro Val Trp Thr Ala Tyr Asn Arg Pro Ala Asp His Phe Glu Ala Arg
                165                 170                 175
Gly Gln Tyr Val Lys Phe Leu Ala Gln Thr Ala
            180                 185
```

<210> 15
<211> 972
<212> DNA
<213> Mouse

<220>
<221> CDS
<222> (17)..(556)

<400> 15

```
agccgccgcc gccacc atg gtg cag gcc tgg tat atg gac gag tcc acc gcc 52
                  Met Val Gln Ala Trp Tyr Met Asp Glu Ser Thr Ala
                    1               5                  10

gac ccg cgg aag ccc cac cgc gca cag ccc gac cgc ccc gtg agc ctg   100
Asp Pro Arg Lys Pro His Arg Ala Gln Pro Asp Arg Pro Val Ser Leu
         15                  20                  25

gag cag ctg cgc acg ctc gga gtg ctc tat tgg aag cta gat gct gac   148
Glu Gln Leu Arg Thr Leu Gly Val Leu Tyr Trp Lys Leu Asp Ala Asp
     30                  35                  40

aag tat gag aac gat cca gaa cta gaa aag atc cgg aaa atg aga aac   196
Lys Tyr Glu Asn Asp Pro Glu Leu Glu Lys Ile Arg Lys Met Arg Asn
 45                  50                  55                  60

tac tcc tgg atg gac atc atc acc ata tgc aaa gat aca ctt ccc aat   244
Tyr Ser Trp Met Asp Ile Ile Thr Ile Cys Lys Asp Thr Leu Pro Asn
```

```
                  65                  70                  75

tac gag gag aag atc aag atg ttc ttt gag gaa cat ctg cat ctg gat   292
Tyr Glu Glu Lys Ile Lys Met Phe Phe Glu Glu His Leu His Leu Asp
             80                  85                  90

gag gag atc cgc tac atc ctg gag ggt agt ggg tac ttc gat gtc agg   340
Glu Glu Ile Arg Tyr Ile Leu Glu Gly Ser Gly Tyr Phe Asp Val Arg
         95                 100                 105

gac aag gag gac aag tgg atc cgg att tcc atg gag aag ggg gac atg   388
Asp Lys Glu Asp Lys Trp Ile Arg Ile Ser Met Glu Lys Gly Asp Met
    110                 115                 120

att act ctt cct gcc ggc atc tat cac cgc ttc aca ctg gac gag aag   436
Ile Thr Leu Pro Ala Gly Ile Tyr His Arg Phe Thr Leu Asp Glu Lys
125                 130                 135                 140

aat tac gtg aag gcc atg cgg ctg ttt gtt gga gaa cct gtg tgg aca   484
Asn Tyr Val Lys Ala Met Arg Leu Phe Val Gly Glu Pro Val Trp Thr
                145                 150                 155

cca tac aac cgg cca gct gac cat ttt gat gcc cgt gta cag tac atg   532
Pro Tyr Asn Arg Pro Ala Asp His Phe Asp Ala Arg Val Gln Tyr Met
            160                 165                 170

agt ttt ttg gaa gga aca gca tag cagtgctcct caaagagaaa actgcactgt  586
Ser Phe Leu Glu Gly Thr Ala
        175                 180

gtgaatctcc tgctgtggta accgaatgga aagttgctca cttttctgct tttgtatttg 646

aacttgaggc tagactagct ctctttgcta ggattgtgag atcagtgtct tttaaatgaa 706

agcctctcta aaagtgagtt ttacatggaa gccacaaaaa tgtgaaaaag tgaccttaat 766

tttccctaac tgtcaagact tagaggtata ggagccctgg attggtatgt gcattcatgc 826

atggccaatc ttcatctccc agatctttag gtgtctgttg gtgtgaagct atgcctcctg 886

caagagggca gttataacca gcacaactaa ccagatgacg tttttctcct ttgctgattg 946

ttgagtgggg aagtggggtt gttgtt                                      972
```

<210> 16
<211> 179
<212> PRT
<213> Mouse

<400> 16

```
Met Val Gln Ala Trp Tyr Met Asp Glu Ser Thr Ala Asp Pro Arg Lys
  1               5                  10                  15
Pro His Arg Ala Gln Pro Asp Arg Pro Val Ser Leu Glu Gln Leu Arg
             20                  25                  30
Thr Leu Gly Val Leu Tyr Trp Lys Leu Asp Ala Asp Lys Tyr Glu Asn
         35                  40                  45
Asp Pro Glu Leu Glu Lys Ile Arg Lys Met Arg Asn Tyr Ser Trp Met
     50                  55                  60
Asp Ile Ile Thr Ile Cys Lys Asp Thr Leu Pro Asn Tyr Glu Glu Lys
 65                  70                  75                  80
```

```
Ile Lys Met Phe Phe Glu Glu His Leu His Leu Asp Glu Glu Ile Arg
                 85                  90                  95
Tyr Ile Leu Glu Gly Ser Gly Tyr Phe Asp Val Arg Asp Lys Glu Asp
            100                 105                 110
Lys Trp Ile Arg Ile Ser Met Glu Lys Gly Asp Met Ile Thr Leu Pro
        115                 120                 125
Ala Gly Ile Tyr His Arg Phe Thr Leu Asp Glu Lys Asn Tyr Val Lys
    130                 135                 140
Ala Met Arg Leu Phe Val Gly Glu Pro Val Trp Thr Pro Tyr Asn Arg
145                 150                 155                 160
Pro Ala Asp His Phe Asp Ala Arg Val Gln Tyr Met Ser Phe Leu Glu
                165                 170                 175
Gly Thr Ala
```

<210> 17
<211> 706
<212> DNA
<213> Zebrafish

<220>
<221> CDS
<222> (36)..(581)
<223> n at positions 634 and 642 is unknown

<400> 17

```
gtactgcgca tggagaccga accggactgt tcaag atg agt gtt ttc gag gca    53
                                        Met Ser Val Phe Glu Ala
                                          1               5

tgg tac atg gat gaa gag tcc gga gag gac cag aga ctc ccg cac aaa   101
Trp Tyr Met Asp Glu Glu Ser Gly Glu Asp Gln Arg Leu Pro His Lys
             10                  15                  20

ctg agc ccg aat cag ccc gtc agc gtc cag cag ctg gag cac atc gga   149
Leu Ser Pro Asn Gln Pro Val Ser Val Gln Gln Leu Glu His Ile Gly
         25                  30                  35

gtc ttt cac tgg aag ctg aac gct gat atc tat gaa aat gac ccc gaa   197
Val Phe His Trp Lys Leu Asn Ala Asp Ile Tyr Glu Asn Asp Pro Glu
     40                  45                  50

ctg cag aag atc cga gag gag aag ggt tat tcc ttt atg gac atc ata   245
Leu Gln Lys Ile Arg Glu Glu Lys Gly Tyr Ser Phe Met Asp Ile Ile
 55                  60                  65                  70

acc att cac ccg gac aaa ctg ccc gat tac caa aac aaa ctg aaa atg   293
Thr Ile His Pro Asp Lys Leu Pro Asp Tyr Gln Asn Lys Leu Lys Met
                 75                  80                  85

ttt tac gaa gag cat ctc cac ctg gac gat gag atc cgt tat att ctg   341
Phe Tyr Glu Glu His Leu His Leu Asp Asp Glu Ile Arg Tyr Ile Leu
             90                  95                 100

gaa gga tcc tct tat ttt gat gtg cgg gac gaa ggc gac cgc tgg atc   389
Glu Gly Ser Ser Tyr Phe Asp Val Arg Asp Glu Gly Asp Arg Trp Ile
         105                 110                 115
```

```
cga ata gcg gtg tct aaa ggc gac ctc atc act tta ccg gcc ggg att   437
Arg Ile Ala Val Ser Lys Gly Asp Leu Ile Thr Leu Pro Ala Gly Ile
    120                 125                 130

tac cac aga ttc acc gtg gac gaa agc aac tac act aaa gcc atg cgt   485
Tyr His Arg Phe Thr Val Asp Glu Ser Asn Tyr Thr Lys Ala Met Arg
135                 140                 145                 150

ctg ttc gtg ggt gaa ccc gtc tgg aag gcc tac aac cgt cca gcc gat   533
Leu Phe Val Gly Glu Pro Val Trp Lys Ala Tyr Asn Arg Pro Ala Asp
                155                 160                 165

gac ttt gac atc cgc aag gaa tac gtg aac tcg ctg gga agc tcc tga   581
Asp Phe Asp Ile Arg Lys Glu Tyr Val Asn Ser Leu Gly Ser Ser
            170                 175                 180

aatgcctgat gggattgatt tagtgctgag aatcagactc tgcggtgcct tanacagaca 641

ngcagcaata gtagagctaa catgtcatta cttagtcatc aagacacacc tgatataaag 701

attat                                                             706
```

<210> 18
<211> 181
<212> PRT
<213> Zebrafish
<223> n at positions 634 and 642 is unknown

<400> 18

```
Met Ser Val Phe Glu Ala Trp Tyr Met Asp Glu Glu Ser Gly Glu Asp
  1               5                  10                  15
Gln Arg Leu Pro His Lys Leu Ser Pro Asn Gln Pro Val Ser Val Gln
             20                  25                  30
Gln Leu Glu His Ile Gly Val Phe His Trp Lys Leu Asn Ala Asp Ile
         35                  40                  45
Tyr Glu Asn Asp Pro Glu Leu Gln Lys Ile Arg Glu Glu Lys Gly Tyr
     50                  55                  60
Ser Phe Met Asp Ile Ile Thr Ile His Pro Asp Lys Leu Pro Asp Tyr
 65                  70                  75                  80
Gln Asn Lys Leu Lys Met Phe Tyr Glu Glu His Leu His Leu Asp Asp
                 85                  90                  95
Glu Ile Arg Tyr Ile Leu Glu Gly Ser Ser Tyr Phe Asp Val Arg Asp
            100                 105                 110
Glu Gly Asp Arg Trp Ile Arg Ile Ala Val Ser Lys Gly Asp Leu Ile
        115                 120                 125
Thr Leu Pro Ala Gly Ile Tyr His Arg Phe Thr Val Asp Glu Ser Asn
    130                 135                 140
Tyr Thr Lys Ala Met Arg Leu Phe Val Gly Glu Pro Val Trp Lys Ala
145                 150                 155                 160
Tyr Asn Arg Pro Ala Asp Asp Phe Asp Ile Arg Lys Glu Tyr Val Asn
                165                 170                 175
Ser Leu Gly Ser Ser
            180
```